

CCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAG  
 AGATGCAAGGGGTGAAGGAGCGCTTCTACCGTTAGGGAACTCTGGGACAGAGCGCCCC  
 GGCGCCTGATGGCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGGAACCATA  
 CCATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGC  
M A R I P K T L K F V V V I V A V L L P  
 CAGTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTCCCCAGCAGACAGTGG  
V L A Y S A T T A R Q E E V P Q Q T V A  
 CCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGAT  
 P Q Q Q R H S F K G E E C P A G S H R S  
 CAGAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCA  
 E H T G A C N P C T E G V D Y T N A S N  
 ACAATGAACCTTCTTGCTTCCATGTACAGTTGTAATCAGATCAAAACATAAAAGTT  
 N E P S C F P C T V C K S D Q K H K S S  
 CCTGCACCATGACCAGAGACACAGTGTGTCAAGTAAAGAAGGCACCTCCGGAATGAAA  
 C T M T R D T V C Q C K E G T F R N E N  
 ACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTA  
 S P E M C R K C S R C P S G E V Q V S N  
 ATTGTACGTCTGGATGATATCCAGTGTGTGAAGAATTGGTGCCAATGCCACTGTGG  
 C T S W D D I Q C V E E F G A N A T V E  
 AAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTG  
 T P A A E E T M N T S P G T P A P A A E  
 AAGAGACAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCA  
 E T M N T S P G T P A P A A E E T M T T  
 CCAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAAGCCGGGACTC  
 S P G T P A P A A E E T M T T S P G T P  
 CTGCCAGCTGCTGAAGAGACAATGACCAAGCCGGGACTCCTGCCCTTCATT  
 A P A A E E T M T T S P G T P A S S H Y

**FIG.1A**

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ACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGTTT  
L S C T I V G I I V L I V L L I V F V \*

GAAAGACTTCACTGTGGAAGAAATTCCCTCCTTACCTGAAAGGTTCAGGTAGGCGCTGGC  
TGAGGGCGGGGGGGCGCTGGACACTCTGCCCTGCCTCCCTGCTGTGTTCCCACAGAC  
AGAAACGCCTGCCCTGCCCAAGTCCTGGTGTCCAGCCTGGCTATCTTCCCT  
GTGATCGTCCATCCCCACATCCCGTGCACCCCCCAGGACCCCTGGTCTCATCAGTCCCTC  
TCCTGGAGCTGGGGTCCACACATCTCCAGCCAAGTCCAAGAGGCAGGGCCAGTTCC  
CCATCTTCAGGCCAGCCAGGCAGGGGGCAGTCGGCTCTCAACTGGGTGACAAGGGTGA  
GGATGAGAAGTGGTCACGGGATTATTACGCCCTGGTCAGAGCAGAACACAGAGATTTC  
CGTAAAAAAA

FIG. 1B

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FIG. 2A

## FIG. 2B

FIG. 2C

FIG. 2D

Consensus #1												
149	-	-	C	L	N	G	T	V	H	L	-	S
141	-	-	K	C	R	P	G	F	G	V	A	R
128	-	-	C	E	A	G	S	G	L	V	-	F
146	-	R	L	V	L	C	Q	P	G	T	E	A
137	-	-	-	-	-	-	-	-	-	S	T	V
87	-	-	C	N	S	G	I	-	L	V	-	R
129	S	V	-	-	C	P	A	G	M	I	V	K
123	R	-	S	C	S	P	G	F	G	V	K	Q
106	-	-	C	K	Q	G	Q	E	L	T	K	G
110	-	-	R	A	G	T	Q	P	I	-	D	S
131	T	-	R	C	G	I	G	Y	G	V	S	G
131	T	-	R	C	G	I	G	Y	G	V	S	G
131	-	-	C	P	S	G	E	V	Q	V	-	S

FIG. 2E

FIG. 2F

FIG. 2G

TNER-like

FIG. 2H

FIG. 21

FIG. 2J

FIG. 2K

		Consensus #1
329	• • • • •	• • • • •
339	• - - - -	L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A T L Y A V V E T N F R L
347	V E K L L	- - - - - D R R A P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S T N F R 2
303	- - - - -	A P S L E E V V L Q Q S P L - - - - -
240	- - - M T L S Q V - - - - -	- - - - - V Q A R E L - - - - -
207	G A L F L - - - - -	- - - - - E A E L I B R
401	S S A F L L C H R R A C R K R I R Q K L H L C Y P V Q T S Q P K L E L V D S R P	- - - - - F A S
252	- - - - -	CD27
216	G R K K L L - - - - -	- - - - - H Q -
245	- - - - -	CD30
281	- - - - -	CD40
284	- - - - -	- - - - - 4-1BB
217	- - - P G T P A P A A E E T M T S P G T P A S - - - - -	- - - - - OX40
		V C 2 2
		C R M B
		T N F R - l i k e

FIG. 2L

FIG. 2M

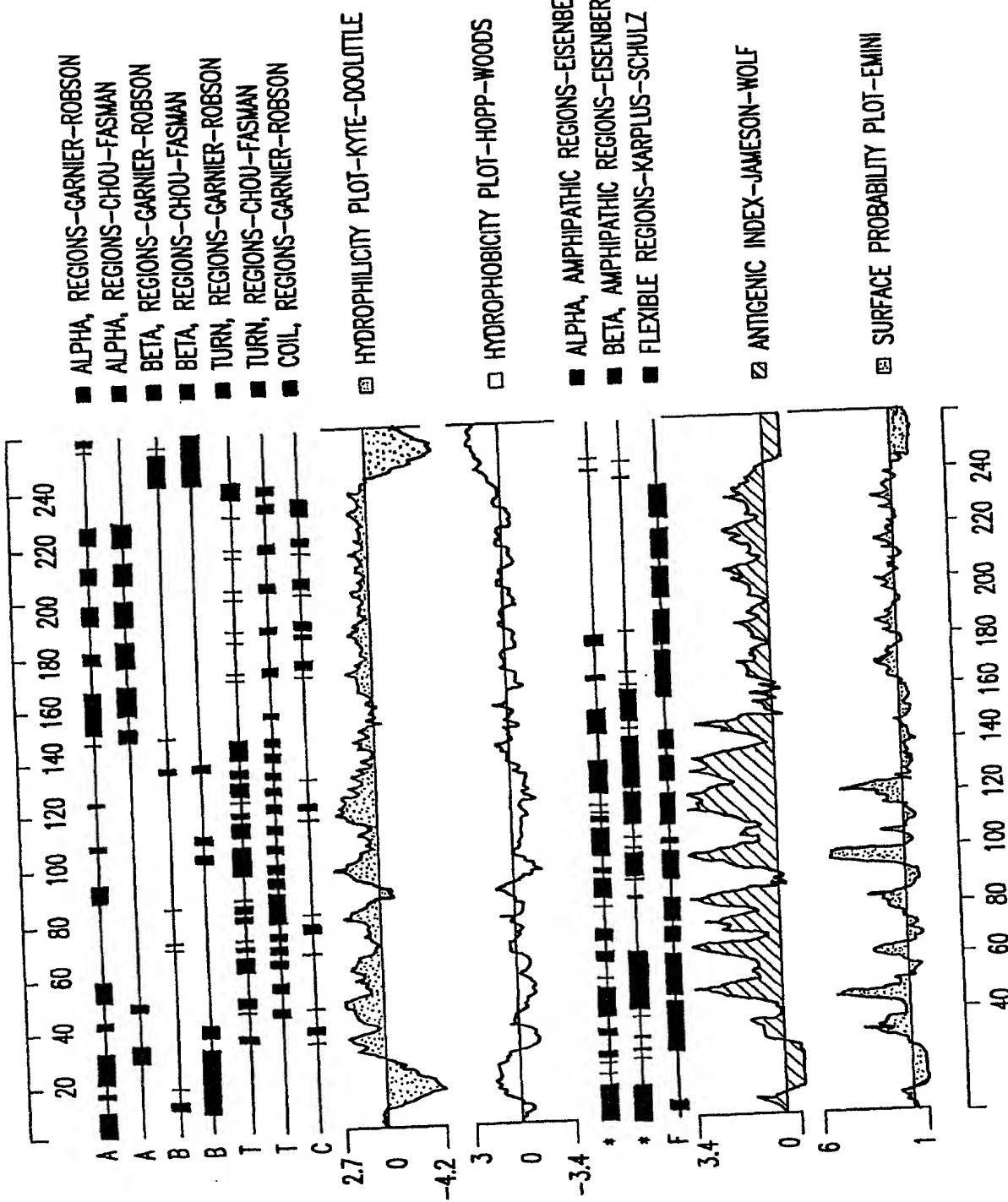
ppl. No. To be assigned; Group Art Unit: To be assigned  
kt. No. 1488.1280006/EKS/EJH;  
ventors: Wei *et al.*; Tel: 202/371-2600  
title: Tumor Necrosis Factor Receptor 5

FIG. 2N

FIG. 20

		Consensus #1	TNFR1	TNFR2	NGFR	LTFR	FAS	CD27	CD30	CD40	4-1BB	OX40	VC22	CRMB	TNFR-like
449	-	· · · · ·	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
448	P	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
413	L	V	E	S	L	C	S	E	S	-	-	-	-	-	-
403	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-
329	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
247	I	Q	E	D	-	Y	R	K	P	-	-	-	-	-	-
560	Y	P	E	Q	E	T	P	P	L	G	S	C	S	D	V
270	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-
236	Q	E	E	D	G	C	-	-	-	S	C	-	-	-	-
263	I	Q	E	E	Q	A	D	A	H	-	-	-	-	-	-
349	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
355	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
258	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

FIG.2P



## HPRCB54R

1 GAATTGGCA NAGCCTCTCC ACGCGCACGA ACTCAGCCAA CGATTTCTGA  
 51 TAGATTTTG GGAGTTGAC CAGAGATGCA AGGGGTGAAG GAGCGCTTCC  
 101 TACCGTTAGG AACTCTGGGG ACAGNNCGCC CCGGCCGCCT GATGGCCGAG  
 151 GCAGGGTGC GACCCAGGACC CAGGACGGCG TCAGGAACCA TACCATGGCC  
 201 CGGATCCCCA AGACCTAAA GTTCGTGGTC GTCATCGTCG CGGTCTGCT  
 251 GCCAGTCCTA GCTTACTCTG CCACCACTGC CCGGCAGAGG AAGTTNCCA  
 301 GCAGNCANTG GNCCCACAGC AACAGNGCA CAGTTCAAG GGGGNAGGAG  
 351 TTTTCCANCA AGTTTTATA GTTCAGAACN TATTGGNGCT NTNAACCCTT  
 401 GCACAAGGGT TTGGNTTAAA CCAANGTTTC CAANATGNAC TTTTTNGTTC  
 451 CCTGTTANAT TTTTTAATTG TTNAAAANTT AAATTNTNA ACCTTNCCNG  
 501 GGNAAATT

## HSJAU57RA

1 GGCAGAGGTG TCTCCAGCCT GGCTCTATCT TCCTCCTTGT NATCGTCCCA  
 51 TCCCCACATC CCGTGCACCC CCCAGGACCC TGGTCTCATC AGTCCCTCTC  
 101 CTGGAGCTGG GGGTCCACAC ATCTCCCAGC CAAGTCCAAG AGGGCAGGGC  
 151 CAGTTCCCTCC CATCTTCAGG CCCAGCCAGG CAGGGGGCAG TCGGCTCCTC  
 201 AACTGGGTGA CAAGGGTGAG GATGAGAAGT GGTCACGGGG ATTTATTCAG  
 251 CCTTGGTCAG AGCAGAACAC AGAGTTTTC CGTGTGTTGG TTTTACTCT  
 301 NNTTCCCCTT CTTNATNCCC CTTTCN

## HUSCB54R

1 CCAGGGTCTC CTNCCCCACC TGCTGAAGAG ACANTGACCA CCAGCCGGGG  
 51 GACTCCTGCC TCTTCCTCAT TACCTCTNAT GNANCATCGT AGGGATCATA  
 101 GTTCTAATTG TGCTTCTGA ATTGTGCTTT GTTTGGAAAG ACTTCACTGT  
 151 GGGAAAGAAAT TCCTTCCTTA CCTGAAGTTG CAGGTAGGCC CTGGGTNAGG  
 201 GCGNGGGCG CTGGACANTN TCTGGNCCTG GCTGCCCGCT G

## HELBP70R

1 GGCAGAGGCC CCAGCTGCTG AAGAGACAAT AATCACCAGC CCGGGGACTC  
 51 CTGNNCTNC TNATTACCTC TNATGCACCA TCGTAGGGAT CATACTTCTA  
 101 ATTGTGCCTT CTAATTGTTT TTGTTGAAA AGANTTCACT GTGGAAGAAA  
 151 TTCTTCCTT ACCTGTAAGT TNCAGGTAGG NGCCTGGCTG AGGGCGGGGG  
 201 GCGCTGGTAC ACTCTCTGAC CCTGCCTCCC TCTGNCTGTT TTCCACAGA  
 251 CAGAAACGCC TGCCCTGNC CCCAAGTTCC TNGTGTGTTTC CAGCCTGGCT  
 301 CTATCTNNC TCCTTGAA TCGTTCCCAT CCCCCACANGC

**FIG.4**

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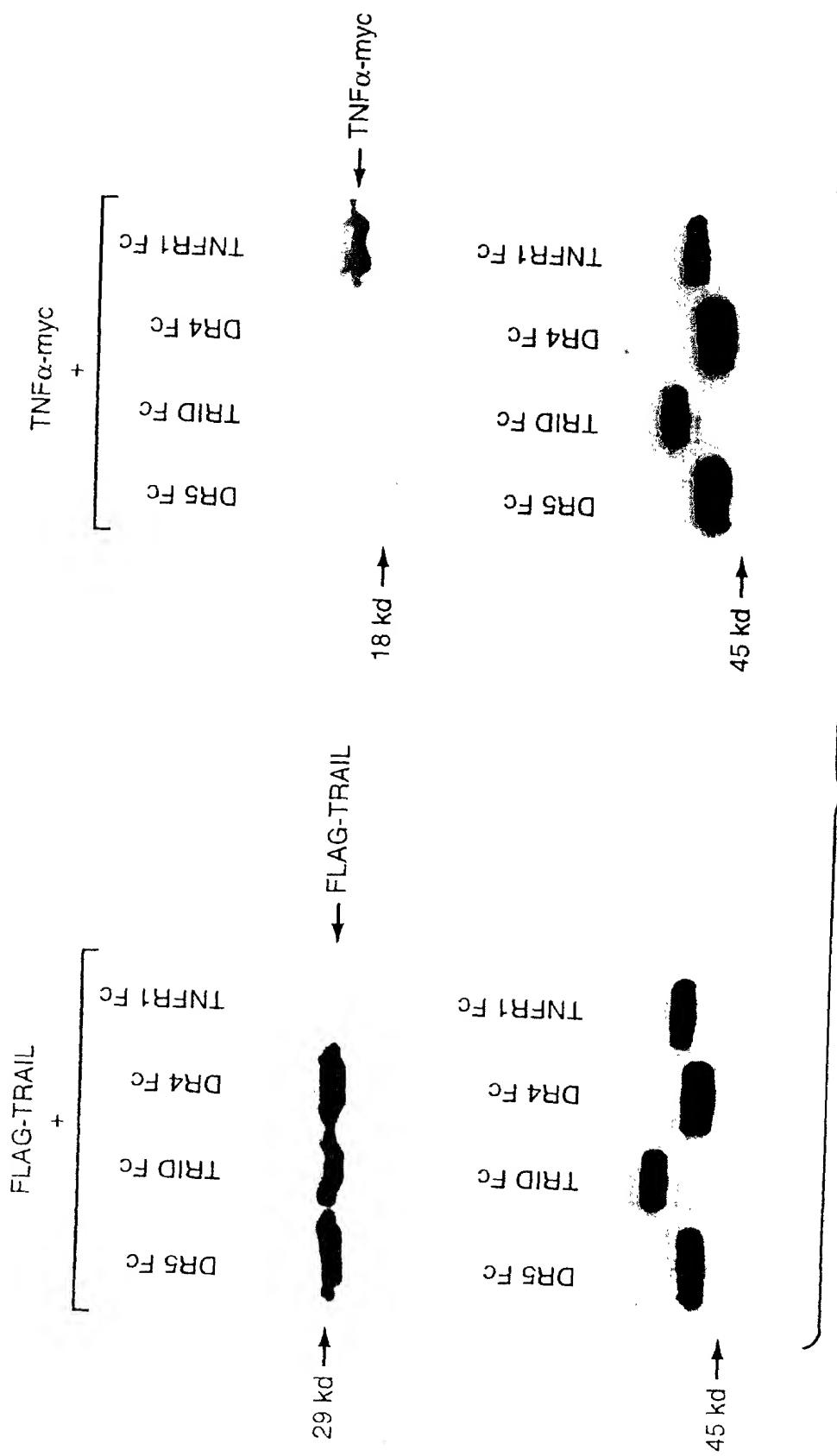


FIG. 5A

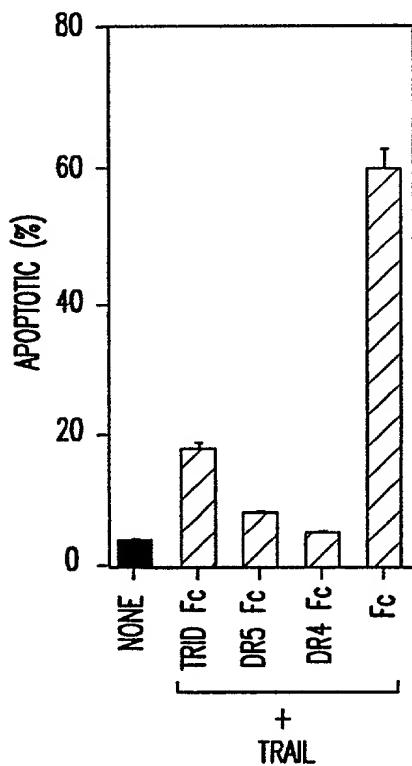


FIG.5B

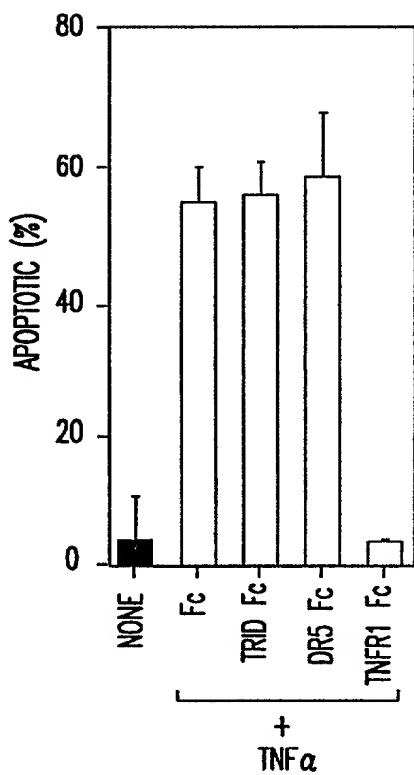


FIG.5C

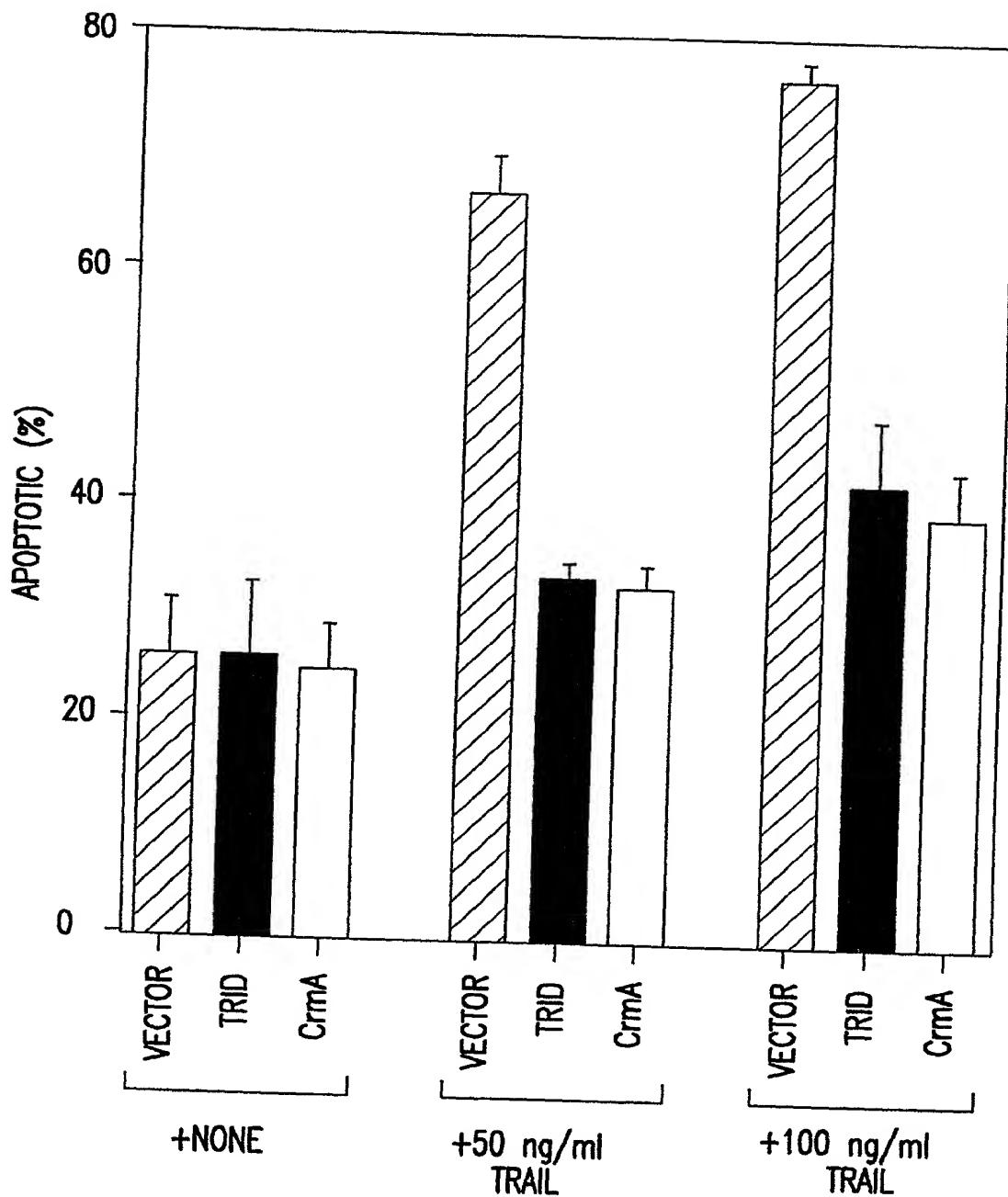


FIG.6